

AMENDMENTS TO THE DRAWINGS

Please replace the drawings with the attached formal drawing sheets (forty-six (46) different sheets, Figs. 1A-9E) submitted herewith.



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

Applicants: Chadwick et al.
Docket No. 28110/36120D
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ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC 60
ATGTGCTTTT TAAATTGGCC TGGGTGACCC GCCCACTTGG TGTAAGAAGAA GAACCGGCCA 120
AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC 180
TCAGGTCCAC ATCTTGGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC 231
Met Ala Thr Ser Trp Gly Ala Val Phe
1 5
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG 279
Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
10 15 20 25
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT 327
Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
30 35 40
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT 375
Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
45 50 55
GGA GCT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG 423
Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
60 65 70

FIG. 1A



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FIG. 1B

ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt	471
Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu	
75 80 85	
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG	519
Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu	
90 95 100 105	
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110 115 120	
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125 130 135	
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT	663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn	
140 145 150	
TCA CCT TTC CTG GTC CCA GAT GGC AGC AGT AGC ATC ATG GAT GGG TCC	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155 160 165	



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FIG. 1C

TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG	759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln	185
170 175 180	
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT	807
Leu His Gly Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly	200
190 195	
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	215
205 210	
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	230
220 225	
TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	245
235 240	
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	265
250 255 260	



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FIG. 1D

ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	270 275 280
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG	1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met	285 290 295
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA	1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	300 305 310
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC AGC TTC TAC GCT TTC TCT	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	315 320 325
TAC TAC TAC GAT GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG	1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	330 335 340 345
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG	1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	350 355 360



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TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG	1335
Cys Asp Asn Leu Gly Ser Phe Ser Gly Ser Pro Phe Leu Cys Met	375
	365
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala	390
	385
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC	1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp	405
	395
	400
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT	1479
Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His	425
	415
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA	1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro	435
	430
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT	1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser	445
	450
	455

FIG. 1E



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FIG. 1F

GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGGTTTT 1629
Gly Lys Ala Trp Pro Glu Thr Arg 465
460

TAGATGAGTC TTGCTCTTGA GCCTAGTGAT TTGGGCTTCA ATGATTGCA CATCTAATGT 1689

GAATAGCTCC TAACCACTTG GTGGGTGCAT GGCTGGCACC AGACTGTAAA TCCTTTGGGA 1749

TTCTTTGTAC AGAGTCCTGC AAAGGAAAAA AGAGAAAAGG TTTGGAACTC CATGCTAGAT 1809

TGCGAGTTCA GAGACAGGTC CCTGGGGACC AAAGAACAAAT CTCGTTTCAA CCCTTGGATG 1869

CCTCATTTGCT TTGAATGGAT TCATTTTTCG TTATAAGCTG ATTTACTGAA ATCCCATAAC 1929

CCATCAATGC TGTTAATTTT TTTCTTCTTA CCCTTATTAC ATTCCCTACC CTAAAAGCCT 1989

GGGGGAAATA CCTGGTTTTC CTTCCCATCT ATAATTGAGA AAGAGGGGGG AAAAGATACT 2049

GTATTAGAAT TTGTGTGATC CTGTGGCACA ATAGATCAAC CAACCCATTT AAAGCTTAAA 2109

AAAAAAAAAA

2119



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peaNTase	1	---MELLIKLITFLFSMPAITS SSQYLGNNLLTSRKIFLKQEEISSYAVVFDAGSTGSR
potapyrase	1	MLNQNSHFIFIIIAIFLVLP LSLSKNVNAQIPLRRHLLSHESE --HYAVIFDAGSTGSR
mNTase	1	MATSWGAVFMIIACVGS TVFYREQQTWFEGVFLSSMCPINVSAGTFYGYIMFDAGSTGTR
YGDPase	1	KTPEDISILPVNDEPGYLQDSKTEQNYPELADAVK QTSQTCSEEHKYVIMIDAGSTGSR
peaNTase	57	IHVYHFNQNLDLLHIGKGV EYVNKI ITPGLSSYANNPEQAAKSLIPLLEQAEDVVPDDLQP
potapyrase	59	VHVFRFDEKLGLLPIGN IEYFMATEPGLSSYAEDPKAAANSLEPLLDGAEGVVPQELQS
mNTase	61	IHVYTFVQKTAGQLP PLEGEIFDSVKPGLSAFVDQPKQGAETVQELLEVAKDSIPRSHWE
YGDPase	61	VHIYKFDVCTS --PPTLLDEKFDHLEPGLSSFD TDVGAANS LDPLLLKVAMNYVPIKARS
peaNTase	117	KTPVRLGATAGLRLLNGDASEKILQSV RDMLSNRSTF -NVQPD AVSIIDGTQEGSYLWVT
potapyrase	119	ETPLELGATAGLRMLKGDAAEKILQAVR NLVKNQSTF -HSKDQWVTILDGTQEGSYMMAA
mNTase	121	RTPVV LKATAGLRLLPEQKAQALLLEVEE IFKN -SPF -LVPDG SVSIMDGSYEGILAWVT
YGDPase	119	CTPVA VXATAGLRLLGDAKSSKILSAVR DHLEKDYPPFPV VEGDGVSIMGGDEEGVFAWIT

FIG. 2A



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peaNTase	176	<u>V</u> <u>N</u> <u>Y</u> <u>A</u> <u>L</u> <u>G</u> <u>N</u> <u>L</u> <u>G</u> <u>K</u> <u>K</u> <u>Y</u> <u>T</u> <u>K</u> - - <u>T</u> <u>V</u> <u>G</u> <u>V</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>V</u> <u>S</u> <u>K</u> <u>K</u> <u>T</u> <u>A</u> <u>K</u> <u>N</u> <u>A</u> <u>P</u> <u>K</u> <u>V</u> <u>A</u> <u>D</u> <u>G</u> <u>D</u> <u>D</u> <u>P</u> <u>Y</u> <u>I</u> <u>K</u> <u>V</u> <u>V</u> <u>L</u> <u>K</u> <u>G</u>
potapyrase	178	<u>I</u> <u>N</u> <u>X</u> <u>L</u> <u>L</u> <u>G</u> <u>N</u> <u>L</u> <u>G</u> <u>K</u> <u>D</u> <u>Y</u> <u>K</u> <u>S</u> - - <u>T</u> <u>T</u> <u>A</u> <u>T</u> <u>I</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u> <u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>I</u> <u>S</u> <u>N</u> <u>E</u> <u>Q</u> <u>F</u> <u>A</u> <u>K</u> <u>A</u> <u>P</u> <u>Q</u> <u>N</u> <u>E</u> <u>D</u> <u>G</u> - <u>E</u> <u>P</u> <u>Y</u> <u>V</u> <u>V</u> <u>Q</u> <u>K</u> <u>H</u> <u>L</u> <u>M</u> <u>S</u>
mNTase	179	<u>V</u> <u>N</u> <u>F</u> <u>L</u> <u>T</u> <u>G</u> <u>Q</u> <u>L</u> <u>H</u> <u>G</u> <u>R</u> <u>G</u> <u>Q</u> <u>E</u> - - <u>T</u> <u>V</u> <u>G</u> <u>T</u> <u>L</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>T</u> <u>F</u> <u>L</u> <u>P</u> <u>Q</u> <u>F</u> <u>E</u> <u>K</u> - - - - <u>T</u> <u>L</u> <u>E</u> <u>Q</u> <u>T</u> <u>P</u> <u>R</u> <u>G</u> <u>Y</u> <u>L</u> <u>T</u> <u>S</u> <u>F</u> <u>E</u> <u>M</u> <u>F</u> <u>N</u>
YGDase	179	<u>T</u> <u>N</u> <u>Y</u> <u>L</u> <u>L</u> <u>G</u> <u>N</u> <u>I</u> <u>G</u> <u>A</u> <u>N</u> <u>G</u> <u>P</u> <u>K</u> <u>L</u> <u>P</u> <u>T</u> <u>A</u> <u>A</u> <u>V</u> <u>F</u> <u>D</u> <u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u> <u>I</u> <u>V</u> <u>F</u> <u>E</u> <u>P</u> - - <u>T</u> <u>F</u> <u>P</u> <u>I</u> <u>N</u> <u>E</u> <u>K</u> <u>M</u> <u>V</u> <u>D</u> <u>G</u> <u>E</u> <u>H</u> <u>K</u> <u>F</u> - - <u>D</u> <u>L</u> <u>K</u> <u>F</u> <u>G</u> <u>D</u>
peaNTase	234	<u>I</u> <u>P</u> <u>Y</u> <u>D</u> <u>L</u> <u>Y</u> <u>V</u> <u>H</u> <u>S</u> <u>Y</u> <u>L</u> <u>H</u> <u>F</u> <u>G</u> <u>R</u> <u>E</u> <u>A</u> <u>S</u> <u>R</u> <u>A</u> <u>E</u> <u>I</u> <u>L</u> <u>K</u> <u>L</u> - - - - - <u>T</u> <u>P</u> <u>R</u> <u>S</u> <u>P</u> <u>N</u> <u>P</u> <u>C</u> <u>L</u> <u>L</u> <u>A</u> <u>G</u> <u>F</u> <u>N</u> <u>G</u> <u>I</u> <u>Y</u>
potapyrase	235	<u>K</u> <u>E</u> <u>Y</u> <u>N</u> <u>L</u> <u>Y</u> <u>V</u> <u>H</u> <u>S</u> <u>Y</u> <u>L</u> <u>N</u> <u>Y</u> <u>G</u> <u>Q</u> <u>L</u> <u>A</u> <u>G</u> <u>R</u> <u>A</u> <u>E</u> <u>I</u> <u>F</u> <u>K</u> <u>A</u> - - - - - <u>S</u> <u>R</u> <u>N</u> <u>E</u> <u>S</u> <u>N</u> <u>P</u> <u>C</u> <u>A</u> <u>L</u> <u>E</u> <u>G</u> <u>C</u> <u>D</u> <u>G</u> <u>Y</u> <u>Y</u>
mNTase	232	<u>S</u> <u>T</u> <u>F</u> <u>K</u> <u>L</u> <u>Y</u> <u>T</u> <u>H</u> <u>S</u> <u>Y</u> <u>L</u> <u>G</u> <u>F</u> <u>G</u> <u>L</u> <u>K</u> <u>A</u> <u>R</u> <u>L</u> <u>A</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> - - - - - <u>L</u> <u>E</u> <u>A</u> <u>K</u> <u>G</u> <u>T</u> - - - - <u>D</u> <u>G</u> <u>H</u> <u>T</u> <u>F</u> <u>R</u> <u>S</u>
YGDase	234	<u>E</u> <u>N</u> <u>Y</u> <u>T</u> <u>L</u> <u>Y</u> <u>Q</u> <u>P</u> <u>S</u> <u>H</u> <u>L</u> <u>G</u> <u>Y</u> <u>G</u> <u>L</u> <u>K</u> <u>E</u> <u>G</u> <u>R</u> <u>N</u> <u>K</u> <u>V</u> <u>N</u> <u>S</u> <u>V</u> <u>L</u> <u>V</u> <u>E</u> <u>N</u> <u>A</u> <u>L</u> <u>K</u> <u>D</u> <u>G</u> <u>K</u> <u>I</u> <u>L</u> <u>K</u> <u>G</u> <u>D</u> <u>N</u> <u>T</u> <u>K</u> <u>T</u> <u>H</u> <u>Q</u> <u>L</u> <u>S</u> <u>S</u> <u>P</u> <u>C</u> <u>L</u> <u>P</u> <u>P</u> <u>K</u> <u>V</u> <u>N</u> <u>A</u> <u>T</u> <u>N</u>
peaNTase	276	<u>T</u> <u>Y</u> <u>S</u> <u>G</u> <u>E</u> <u>E</u> <u>F</u> <u>K</u> <u>A</u> <u>T</u> <u>A</u> <u>Y</u> <u>T</u> <u>S</u> <u>G</u> <u>A</u> - - - - - <u>N</u> <u>F</u> <u>N</u> <u>K</u> <u>C</u> <u>K</u> <u>N</u> <u>T</u> <u>I</u> <u>R</u> <u>K</u> <u>A</u> <u>L</u> <u>K</u> <u>L</u> <u>N</u> <u>Y</u> <u>P</u> <u>C</u> <u>P</u> <u>Y</u> <u>Q</u> <u>N</u> <u>C</u> <u>T</u> <u>F</u> <u>G</u> <u>G</u> <u>I</u> <u>N</u> <u>G</u> <u>G</u> <u>G</u> <u>N</u> - - -
potapyrase	277	<u>S</u> <u>Y</u> <u>G</u> <u>G</u> <u>V</u> <u>D</u> <u>Y</u> <u>K</u> <u>V</u> <u>K</u> <u>A</u> <u>P</u> <u>K</u> <u>K</u> <u>S</u> - - - - - <u>S</u> <u>W</u> <u>K</u> <u>R</u> <u>C</u> <u>R</u> <u>R</u> <u>L</u> <u>T</u> <u>R</u> <u>H</u> <u>A</u> <u>L</u> <u>K</u> <u>I</u> <u>N</u> <u>A</u> <u>K</u> <u>C</u> <u>H</u> <u>I</u> <u>E</u> <u>E</u> <u>C</u> <u>T</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>W</u> <u>N</u> <u>G</u> <u>G</u> <u>G</u> <u>D</u> - - -
mNTase	270	<u>A</u> <u>C</u> <u>L</u> <u>P</u> <u>R</u> <u>W</u> <u>L</u> <u>E</u> <u>A</u> <u>E</u> <u>W</u> <u>I</u> <u>F</u> <u>G</u> <u>C</u> <u>V</u> - - - - - <u>K</u> <u>Y</u> <u>Q</u> <u>Y</u> <u>G</u> <u>G</u> <u>N</u> <u>Q</u> <u>E</u> <u>G</u> <u>E</u> <u>M</u> <u>G</u> <u>F</u> <u>E</u> <u>P</u> <u>C</u> <u>Y</u> <u>A</u> <u>E</u> <u>V</u> <u>L</u> <u>R</u> <u>V</u> <u>V</u> <u>Q</u> <u>G</u> <u>K</u> <u>L</u> <u>H</u> <u>Q</u> <u>P</u> <u>E</u> <u>E</u> <u>V</u> <u>R</u> - - -
YGDase	294	<u>E</u> <u>K</u> <u>V</u> <u>T</u> <u>L</u> <u>E</u> <u>S</u> <u>K</u> <u>E</u> <u>T</u> <u>Y</u> <u>T</u> <u>I</u> <u>D</u> <u>F</u> <u>I</u> <u>G</u> <u>P</u> <u>D</u> <u>E</u> <u>P</u> <u>S</u> <u>G</u> <u>A</u> <u>Q</u> <u>C</u> <u>R</u> <u>F</u> <u>L</u> <u>T</u> <u>D</u> <u>E</u> <u>I</u> <u>L</u> <u>N</u> <u>K</u> <u>D</u> <u>A</u> <u>Q</u> <u>C</u> <u>Q</u> <u>S</u> <u>P</u> <u>P</u> <u>C</u> <u>S</u> <u>F</u> <u>N</u> <u>G</u> <u>V</u> <u>H</u> <u>Q</u> <u>P</u> <u>S</u> <u>L</u> <u>V</u> <u>R</u> <u>T</u> <u>F</u> <u>K</u>

FIG. 2B



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peaNTase 328 GQKNLFASSFFYLPEDTGMVDASTPNFILRPVDIETKAKEACALNFEDAKSTYFFLDKK
potapyrase 329 GQKNIHASSPFYDIGAQVGIVDTKFPSALAKPIQYLNAAKVACQTNVADIKSIFPKTQDR
mNTase 322 GSA-FYAFSYVDRAADTHLIDYE-KGGVLKVEDFERKAREVCD-NLGSFSSGSP
YGDase 354 ESNDIYIFSYFYDRTRPLGMPLSFTLNELDLARIVCKGEETWNSVPSGIAGS
peaNTase 388 NVASYVCMDLIYQYVLLVDGFGLDPLQKITSGKEIEYQDAIVEAAWPLGNAVEAISALPK
potapyrase 389 NI-PYLCMDLIYEYTLLVDGFGLNPHKEITVIHDVQYKNYLVGAAWPLGCAIDLVSSTN
mNTase 374 FLCMDLYITALLKDGLGFAERHPLTANKESEQHRDWLGLGHLSPAPVSGHHQLR
YGDase 411 ESDSHFCLDLSFQVSLLHTGYDIPLQRELRTGKKIANKE
peaNTase 448 FERLMYFV
potapyrase 448 KIRVASS*
mNTase 430 PSSTSEACISEPVFPSQEGVDSETFSDLSGKAWPETR*
YGDase 467 KCKIQSA

FIG. 2C



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CD39	1	VKYGIVL	DAGSSHTS	LYIYKW	PAEKENDTGV	VHQVEECRVK	GPGIS
ratCD39	1	VKYGIVL	DAGSSHTN	LYIYKW	PAEKENDTGV	VQLLEECQVK	GPGIS
CD39L1	1	LKYGIVL	DAGSSHTS	MPFIYKW	PADKENDTGI	VGQHSSCDVP	GGGIS
chiATPase	1	FKYGIVL	DAGSSHTA	VFIYKW	PADKENDTGV	VSEHSMCDVE	GPGIS
peaNTase	1	SSYAVVF	DAGSTGSR	IHVYHF	NQ-NLDLLHIGKVEYN	KITPGLS	
potRRORP1	1	KHYAVIF	DAGSTGSR	VHVFRP	DE-KLGLLPIGNNIEYFM	ATEPGLS	
YGDAI	1	HKYVIMI	DAGSTGSR	VHIYKP	DVCTSP	PTLLD-EKFD	MLEPGLS
mNTase	1	TFYGI MF	DAGSTGTR	IHVYTF	VQKTAGQLPFL EG	EIFD	SVKPGLS
hCD39L2	1					FK	ALKPGLS
celegans	1	IKYGVIC	DAGSSGTR	LFVYTLKPLSGGL	TNIDT	L	IHESEPVVKVTPGLS
y71KD	1	DRFGIVL	DAGSSGSR	IHVFKWQDTESSL	LHATNQDSQSILQSVPH	IHQEKDWTFFKLNPGLS	

FIG. 3A



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

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ACR II

CD39	47	KY-VQKVNEIGI-YLTDCMERAREV	IPR---S-QHQETPVYLGATAGMRLLRMES	EEELAD
ratCD39	47	KY-AQKTDEIAA-YLAECMKMSTER	IPAAA-SKQHQ-TPVYLGATAGMRLLRMES	KQSAD
CD39L1	47	SY-ADNPSGASQ-SLVGCLQALQDV	PK---ER-HAGTPLYLGATAGMRLLNL	TNPEAST
chiATPase	47	SY-SSKPPAAGK-SLEHCLSQAMRD	VPK---EK-HADTPLYLGATAGMRLLT	IADPPSQT
peanTPase	46	SY-ANNPEQAAS-LIPLLEQAEDV	VP---DDLQPKTPVRLGATAGLRLLN	--GDA-SE
potRRORP1	46	SY-AEDPKAAANS-LEPLLDGAE	GVVP---QELQSETPLELGATAGLRMLK	--GDA-AE
YGDA1	44	SFDTDSV-GAANS-LDPILLKVAMN	YVPI---KARSCTPVAVKATAGLRLL	--GDAKSS
mNTase	46	AF-VDPQPKQGAET-VQELLEVA	KDSIPRSHWE--R--TPVVVKATAGLRLL	--PEQKAQ
hCD39L2	10	AY-ADDVEKSAQG-IRELLDVAK	QDIP---FDSGRP-TPLVVKATAGLRLL	--PGEKAQ
celegans	51	SFG-DKPEQVVE-YLTPLRRFAE	ENIPLYEQLGE---TDLLIFATAGMRLL	--PEAQKD
Y71KD	61	SFE-KKPPQDAVKSHIKPILLD	FAKNIIPESHWSS---CPVFIQATAGMRLL	--PQDIQS

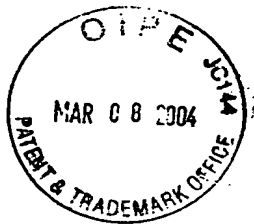
FIG. 3B



Title: METHODS AND COMPOSITIONS
RELATING TO CD-39-LIKE POLYPEPTIDES
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		ACR III			
CD39	101	<u>R</u> <u>V</u> <u>L</u> <u>D</u> <u>V</u> <u>V</u> <u>E</u> <u>R</u> <u>S</u> <u>L</u> <u>S</u> <u>N</u> - <u>Y</u> <u>P</u> <u>P</u>	<u>Q</u> <u>E</u> <u>E</u> <u>G</u> <u>A</u> <u>Y</u> <u>G</u> <u>W</u> <u>I</u> <u>T</u> <u>I</u> <u>N</u>	<u>Y</u> <u>L</u> <u>L</u> <u>G</u> <u>K</u> <u>P</u> <u>S</u> <u>Q</u> <u>K</u> <u>T</u> <u>R</u> <u>W</u> <u>F</u> <u>S</u> <u>I</u> <u>V</u> <u>P</u>	
ratCD39	101	<u>E</u> <u>V</u> <u>L</u> <u>A</u> <u>A</u> <u>V</u> <u>S</u> <u>R</u> <u>S</u> <u>L</u> <u>K</u> <u>S</u> - <u>Y</u> <u>P</u> <u>P</u>	<u>Q</u> <u>E</u> <u>E</u> <u>G</u> <u>A</u> <u>Y</u> <u>G</u> <u>W</u> <u>I</u> <u>T</u> <u>I</u> <u>N</u>	<u>Y</u> <u>L</u> <u>L</u> <u>G</u> <u>R</u> <u>P</u> <u>T</u> <u>Q</u> <u>E</u> <u>Q</u> <u>S</u> <u>W</u> <u>L</u> <u>N</u> <u>F</u> <u>I</u> <u>S</u>	
CD39L1	101	<u>S</u> <u>V</u> <u>L</u> <u>M</u> <u>A</u> <u>V</u> <u>T</u> <u>H</u> <u>T</u> <u>L</u> <u>T</u> <u>Q</u> - <u>Y</u> <u>P</u> <u>P</u>	<u>Q</u> <u>E</u> <u>E</u> <u>G</u> <u>V</u> <u>F</u> <u>G</u> <u>W</u> <u>T</u> <u>A</u>	<u>N</u> <u>Y</u> <u>L</u> <u>L</u> <u>E</u> <u>N</u> <u>F</u> <u>I</u> - <u>K</u> <u>Y</u> <u>G</u> <u>W</u> <u>V</u> <u>G</u> -- <u>R</u>	
chiATPase	101	- <u>C</u> <u>L</u> <u>S</u> <u>A</u> <u>V</u> <u>M</u> <u>A</u> <u>T</u> <u>L</u> <u>K</u> <u>S</u> - <u>Y</u> <u>P</u> <u>P</u>	<u>Q</u> <u>E</u> <u>E</u> <u>G</u> <u>V</u> <u>F</u> <u>G</u> <u>W</u> <u>I</u> <u>T</u> <u>A</u>	<u>N</u> <u>Y</u> <u>L</u> <u>L</u> <u>E</u> <u>N</u> <u>F</u> <u>I</u> - <u>K</u> <u>R</u> <u>G</u> <u>W</u> <u>L</u> <u>G</u> -- <u>E</u>	
peaNTase	97	<u>K</u> <u>I</u> <u>L</u> <u>Q</u> <u>S</u> <u>V</u> <u>R</u> <u>D</u> <u>M</u> <u>L</u> <u>S</u> <u>N</u> <u>R</u> <u>S</u> <u>T</u> <u>F</u> <u>N</u> - <u>V</u> <u>Q</u> <u>P</u> <u>D</u> - <u>A</u> - <u>V</u> <u>S</u> <u>I</u> <u>I</u> <u>D</u> <u>G</u>	<u>T</u> <u>Q</u> <u>E</u> <u>G</u> <u>S</u> <u>Y</u> <u>L</u> <u>W</u> <u>V</u> <u>T</u> <u>V</u>	<u>N</u> <u>Y</u> <u>A</u> <u>L</u> <u>G</u> <u>N</u> -- <u>L</u> -- <u>G</u>	
potRROP1	97	<u>K</u> <u>I</u> <u>L</u> <u>Q</u> <u>A</u> <u>V</u> <u>R</u> <u>N</u> <u>L</u> <u>V</u> <u>K</u> <u>N</u> <u>Q</u> <u>S</u> <u>T</u> <u>F</u> <u>H</u> -- <u>S</u> <u>K</u> <u>D</u> - <u>Q</u> <u>W</u> <u>V</u> <u>T</u> <u>I</u> <u>L</u> <u>D</u> <u>G</u>	<u>T</u> <u>Q</u> <u>E</u> <u>G</u> <u>S</u> <u>Y</u> <u>M</u> <u>W</u> <u>A</u> <u>I</u>	<u>N</u> <u>Y</u> <u>L</u> <u>L</u> <u>G</u> <u>N</u> -- <u>L</u> -- <u>G</u>	
yGDA1	95	<u>K</u> <u>I</u> <u>L</u> <u>S</u> <u>A</u> <u>V</u> <u>R</u> <u>D</u> <u>H</u> <u>L</u> <u>E</u> <u>K</u> <u>D</u> <u>Y</u> <u>P</u> <u>P</u> <u>P</u> <u>V</u> <u>E</u> <u>G</u> <u>D</u> - <u>G</u> - <u>V</u> <u>S</u> <u>I</u> <u>M</u> <u>G</u> <u>G</u>	<u>D</u> <u>E</u> <u>E</u> <u>G</u> <u>V</u> <u>F</u> <u>A</u> <u>W</u> <u>I</u> <u>T</u> <u>T</u>	<u>N</u> <u>Y</u> <u>L</u> <u>L</u> <u>G</u> <u>N</u> -- <u>I</u> <u>G</u> <u>A</u> <u>N</u> <u>G</u>	
mNTase	97	<u>A</u> <u>L</u> <u>L</u> <u>L</u> <u>E</u> <u>V</u> <u>E</u> <u>E</u> <u>I</u> <u>F</u> - <u>K</u> <u>N</u> <u>S</u> <u>P</u> <u>P</u> - <u>L</u> <u>V</u> - <u>P</u> <u>D</u> - <u>G</u> <u>S</u> <u>V</u> <u>S</u> <u>I</u> <u>M</u> <u>D</u> <u>G</u> <u>S</u>	<u>S</u> <u>E</u> <u>G</u> <u>I</u> <u>L</u> <u>A</u> <u>W</u> <u>V</u> <u>T</u> <u>V</u>	<u>N</u> <u>F</u> <u>L</u> <u>T</u> <u>G</u> <u>Q</u> -- <u>L</u> <u>H</u> <u>G</u> <u>R</u> <u>G</u>	
hCD39L2	61	<u>K</u> <u>L</u> <u>L</u> <u>Q</u> <u>K</u> <u>V</u> <u>K</u> <u>E</u> <u>Y</u> <u>L</u> - <u>K</u> <u>H</u> <u>S</u> <u>P</u> <u>P</u> - <u>L</u> <u>V</u> - <u>G</u> <u>D</u> - <u>D</u> <u>C</u> <u>V</u> <u>S</u> <u>I</u> <u>M</u> <u>N</u> <u>G</u> <u>T</u> <u>D</u>	<u>E</u> <u>G</u> <u>V</u> <u>S</u> <u>A</u> <u>W</u> <u>X</u> <u>T</u> <u>I</u>	<u>N</u> <u>F</u> <u>L</u> <u>T</u> <u>G</u> <u>S</u> -- <u>L</u> <u>K</u> <u>T</u> <u>P</u> <u>G</u>	
celegans	102	<u>A</u> <u>I</u> <u>I</u> <u>K</u> <u>N</u> <u>L</u> <u>Q</u> <u>N</u> <u>G</u> <u>L</u> <u>K</u> <u>S</u> <u>V</u> <u>T</u> <u>A</u> <u>L</u> <u>R</u> <u>V</u> <u>S</u> <u>D</u> -- <u>S</u> <u>N</u> <u>I</u> <u>R</u> <u>I</u> <u>D</u> <u>G</u> <u>A</u> <u>W</u>	<u>E</u> <u>G</u> <u>I</u> <u>Y</u> <u>S</u> <u>W</u> <u>I</u> <u>A</u> <u>V</u>	<u>N</u> <u>Y</u> <u>I</u> <u>L</u> <u>G</u> <u>R</u> -- <u>F</u> <u>D</u> --	
y71KD	113	<u>S</u> <u>I</u> <u>L</u> <u>D</u> <u>G</u> <u>L</u> <u>C</u> <u>Q</u> <u>G</u> <u>L</u> <u>K</u> <u>H</u> <u>P</u> <u>A</u> <u>E</u> <u>F</u> <u>L</u> <u>V</u> <u>E</u> <u>D</u> <u>C</u> <u>S</u> - <u>A</u> <u>Q</u> <u>I</u> <u>Q</u> <u>V</u> <u>I</u> <u>D</u> <u>G</u> <u>E</u> <u>T</u>	<u>E</u> <u>G</u> <u>L</u> <u>Y</u> <u>G</u> <u>W</u> <u>L</u> <u>G</u> <u>I</u>	<u>N</u> <u>Y</u> <u>L</u> <u>Y</u> <u>G</u> <u>H</u> -- <u>F</u> <u>N</u> <u>D</u> <u>Y</u> <u>N</u>	

FIG. 3C



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ACR IV				
CD39	155	<u>Y</u> <u>E</u> <u>T</u> <u>N</u> <u>N</u> <u>Q</u> <u>E</u> <u>T</u> <u>F</u> <u>G</u> <u>A</u> <u>L</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u>	<u>V</u> <u>T</u> <u>F</u> <u>V</u> <u>P</u> <u>Q</u> <u>N</u> <u>Q</u>
ratCD39	155	- <u>D</u> <u>S</u> <u>Q</u> <u>K</u> <u>Q</u> <u>A</u> <u>T</u> <u>F</u> <u>G</u> <u>A</u> <u>L</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>S</u> <u>T</u> <u>Q</u>	<u>V</u> <u>T</u> <u>F</u> <u>V</u> <u>P</u> <u>L</u> <u>N</u> <u>Q</u>
CD39L1	152	<u>W</u> <u>F</u> <u>R</u> <u>P</u> <u>R</u> <u>K</u> <u>G</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> <u>M</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u>	<u>I</u> <u>T</u> <u>F</u> <u>E</u> <u>T</u> <u>T</u> <u>S</u> <u>P</u>
chiATPase	151	<u>W</u> <u>I</u> <u>Q</u> <u>S</u> <u>K</u> <u>K</u> <u>T</u> <u>L</u> <u>G</u> <u>A</u> <u>M</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u>	<u>I</u> <u>T</u> <u>F</u> <u>E</u> <u>T</u> <u>S</u> <u>D</u> <u>A</u> <u>I</u>
peanTPase	144	<u>K</u> <u>K</u> <u>Y</u> <u>T</u> <u>K</u> - - <u>T</u> <u>V</u> <u>G</u> <u>V</u> <u>I</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u>	<u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>V</u> <u>S</u> <u>K</u> <u>K</u>
potRROP1	144	<u>K</u> <u>D</u> <u>Y</u> <u>K</u> <u>S</u> - - <u>T</u> <u>T</u> <u>A</u> <u>T</u> <u>I</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>V</u> <u>Q</u>	<u>M</u> <u>A</u> <u>Y</u> <u>A</u> <u>I</u> <u>S</u> <u>N</u> <u>E</u>
YGDAl	146	<u>P</u> <u>K</u> <u>L</u> - <u>P</u> - - <u>T</u> <u>A</u> <u>A</u> <u>V</u> <u>F</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u>	<u>I</u> <u>V</u> <u>F</u> <u>E</u> <u>P</u> <u>T</u> <u>F</u> <u>P</u> <u>I</u>
mNTPase	146	<u>Q</u> <u>E</u> - - - - <u>T</u> <u>V</u> <u>G</u> <u>T</u> <u>L</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u>	<u>I</u> <u>T</u> <u>F</u> <u>L</u> <u>P</u> <u>Q</u> <u>F</u> <u>E</u>
hCD39L2	110	<u>G</u> <u>S</u> - - - - <u>S</u> <u>V</u> <u>G</u> <u>M</u> <u>L</u> <u>D</u>	<u>L</u> <u>G</u> <u>G</u> <u>S</u> <u>T</u> <u>Q</u>	<u>I</u> <u>A</u> <u>F</u> <u>L</u> <u>P</u> <u>R</u> <u>V</u> <u>E</u>
celegans	149	<u>K</u> <u>E</u> - <u>N</u> <u>D</u> <u>S</u> - <u>K</u> <u>V</u> <u>G</u> <u>M</u> <u>I</u> <u>D</u>	<u>M</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>V</u> <u>Q</u>	<u>I</u> <u>A</u> <u>F</u> <u>E</u> <u>I</u> <u>A</u> - <u>N</u> <u>E</u>
Y71KD	165	<u>P</u> <u>E</u> <u>V</u> <u>S</u> <u>D</u> <u>H</u> <u>P</u> <u>T</u> <u>F</u> <u>G</u> <u>F</u> <u>M</u> <u>D</u>	<u>M</u> <u>G</u> <u>G</u> <u>A</u> <u>S</u> <u>T</u> <u>Q</u>	<u>I</u> <u>A</u> <u>F</u> - - <u>A</u> <u>P</u> <u>H</u> <u>D</u> <u>S</u>

FIG. 3D

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RELATING TO CD-39-LIKE POLYPEPTIDES
AND NUCLEIC ACIDS

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GTGGGGTCGT ATCCCGCGGG TGGAGCGCGG GGTGGCGCGG GCCGGGCGG GGGAGCCCA 60
AAGACCGGCT GCCGCCTGCT CCCCCGAAA GGCACACTCGT CTCCGTGGGT GTGGCGGAGC 120
GCGCGGTGCA TGGAAATGGC TATGTGAATG AAAAAAGTA TCCGTTATGA AACTTCCAGA 180
AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GSCAAACAAG G ATG AGA 237
Met Arg
1
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC 285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
5 10 15
CTG GGG CTG TGT GTG GGC GTG PTC ATC TAT GTT GCC TAC ATC AAG TGG 333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
20 25 30
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC 381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
35 40 45 50

FIG. 4A



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CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT 429
Pro Gly Ala Arg Trp Gly Gln Ala His Ser Pro Leu Gly Thr Ala 65
55 60
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC 477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser 80
70 75
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA 525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu 95
85 90
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT 573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu 110
100 105
TCT GCC TAT GCT GAT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA 621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu 125
115 120 130

FIG. 4B



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AND NUCLEIC ACIDS

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CTA CTG GAT GTT GCT AAA CAG GAC GAC ATT CCG TTC GAC TTC TGG AAG GCC Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala 135 140 145	669
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly 150 155 160	717
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA Glu Lys Ala Gln Lys Leu Lys Leu Gln Lys Val Lys Glu Val Phe Lys Ala 165 170 175	765
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr 180 185 190	813
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser 195 200 205 210	861
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA Leu Lys Thr Pro Gly Gly Ser Val Gly Met Leu Asp Leu Gly Gly 215 220 225	909

FIG. 4C



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GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG 957
Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
230 235 240

GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC 1005
Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
245 250 255

TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA 1053
Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Met Ser Ala
260 265 270

CGC CTG GCG ATC CTG GGC GGC GTG GAG GGC CAG CCT GCT AAG GAT GGA 1101
Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
275 280 285 290

AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG 1149
Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
295 300 305

GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA 1197
Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
310 315 320

FIG. 4D



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AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC 1245
Ser. Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 335
325 330

ACA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC 1293
Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 350
340 345

TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG 1341
Ser Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 365
355 360

AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC 1389
Lys Gly Gly Ser Leu Val Val Glu Phe Glu Ile Ala Ala Lys Tyr 380
375 385

GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC 1437
Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 395
390 400

ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC 1485
Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro 410
405 415



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AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC 1533
Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
420 425 430

AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA 1581
Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
435 440 445 450

CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG 1629
Gln Lys Ser Pro Ala Ser
455

CAGTGTCTGT GTGTCTGCAAT AAACCCCTCCT GTCCCTGGACG TGA CTTTCATC CTGAGGAGCC 1689

ACAGCACAGG CCGTGCTGGC ACTTTCIGCA CACTGGCTCT GGGACTTGCA GAAGGCCCTGG 1749

TGCTGCCCCTG GCATCAGCCT CTTCCAGTCA CATCTGGCCA GAGGGCTGTC TGGACCTGGG 1809

CCCTGCTCAA TGCCACCTGT CTGCCCTGGG TCCAAGTGGG CAGGACCAGG ACAGAACCAC 1869

AGGCACACAC TGAGGGGGCA GTGTGGCTCC CTGCCTGTCC CATCCCCATG CCCCCTCCGC 1929

FIG. 4F



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GGGGCTGTGG CTGCTGCTGT GCATGTCCCT GCGATGGGAG TCTTGCTCC CAGCCTGTCA 1989
GTTTCCTCCC CAGGGCAGAG CTCCCCCTCC TGCAAGAGTC TGGAGGCGG TGCAGGCTGT 2049
CCTGGCTGCT CTGGGGAAGC CGAGGGACAG CCATAACACC CCCGGGACAG TAGGTCTGGG 2109
CGGCACCACT GGGAACTCTG GACTTGAGTG TGTTGCTCT TCCTTGGGTA TGAATGTGTG 2169
AGTTCACCCA GAGGCCTGCT CTCCTCACAC ATTGTGTGGT TTGGGGTTAA TGATGGAGGG 2229
AGACACCTCT TCATAGACGG CAGGTGCCCCA CCTTTCAGGG AGTCTCCCAG CATGGGCGGA 2289
TGCCGGGCAT GAGCTGCTGT AAATATTG TGGCTGTGCT GCTTGAGTGA CGTCTCTGTC 2349
GTGTGGGTGC CAAGTGCTTG TGTAGAAACT GTGTTCTGAG CCCCCTTTC TGGACACCAA 2409
CTGTGTCCCTG TGAATGTATC GCTACTGTGA GCTGTTCCCG CCTAGCCAGG GCCATGTCTT 2469
AGGTGCAGCT GTGCCACGGG TCAGCTGAGC CACAGTCCCA GAACCAAGCT CTCGGTGTCT 2529

FIG. 4G



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CGGGCCACCA TCGGGCCACC TCGGGCTGAC CCCACCTCCT CCATGGACAG TGTGAGCCCC 2589
GGGCGGTGCA TCCTGCTCAG TGTGGCGTCA GTGTCGGGGC TGAGCCCCCTT GAGCTGCTTC 2649
AGTGAATGTA CAGTGCCCGG CACGAGCTGA ACCTCATGTG TTCCACTCCC AATAAAAGGT 2709
TGACAGGGGC TTCTCCTTCA AAAAAAAAAA AAAAAAAAAA AAA 2762

FIG. 4H



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FIG. 5A

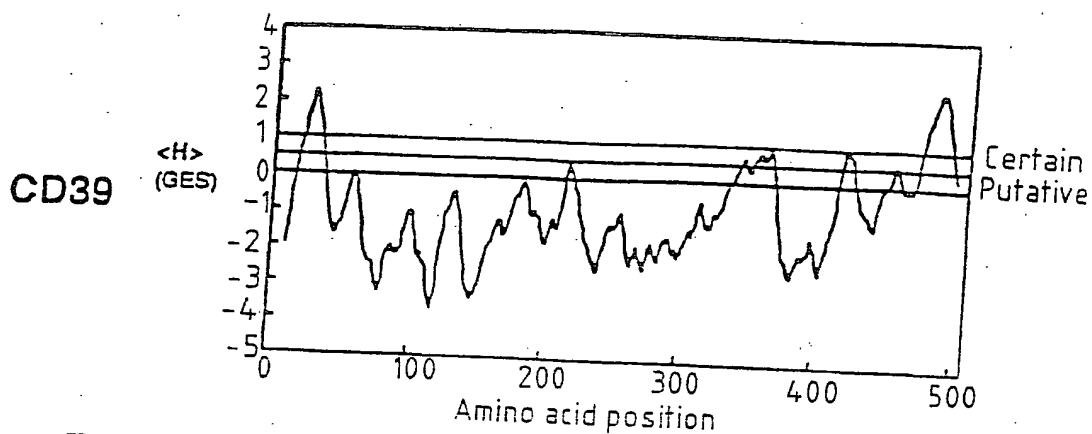


FIG. 5B

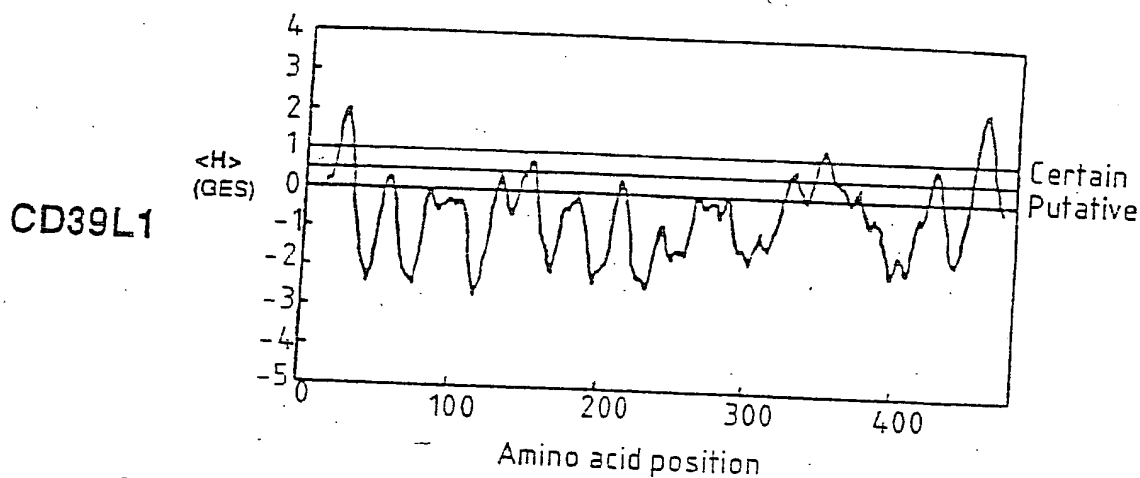
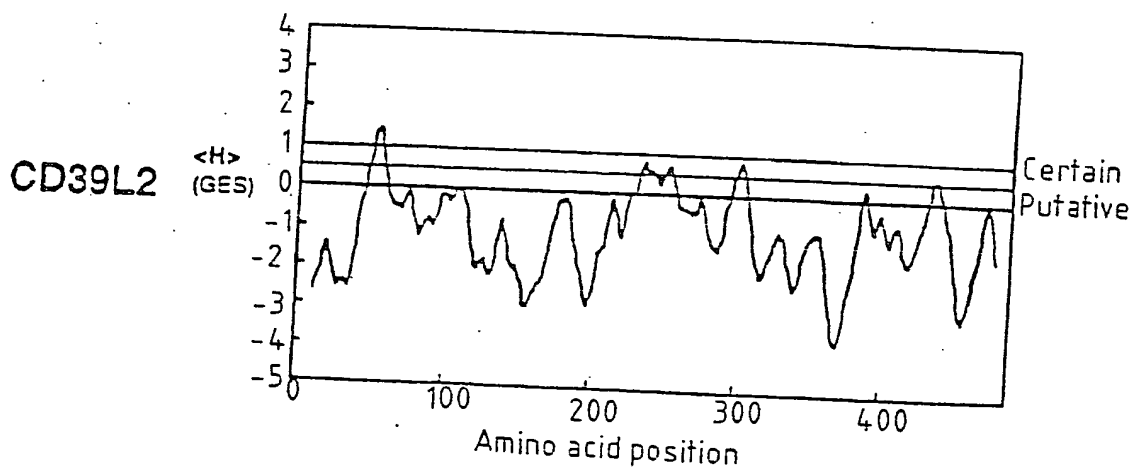
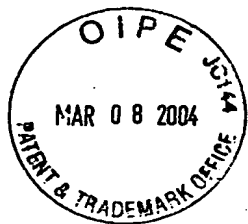


FIG. 5C





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FIG. 5D

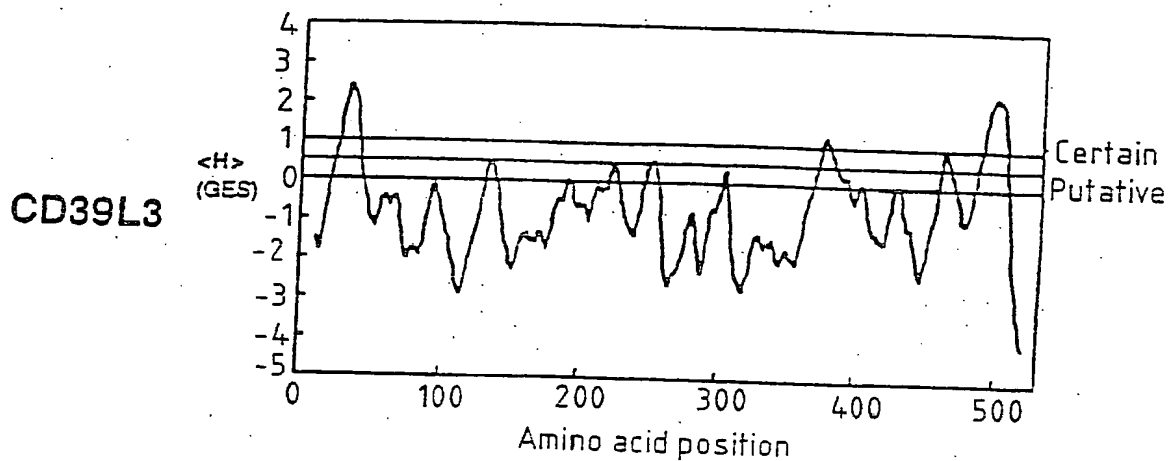
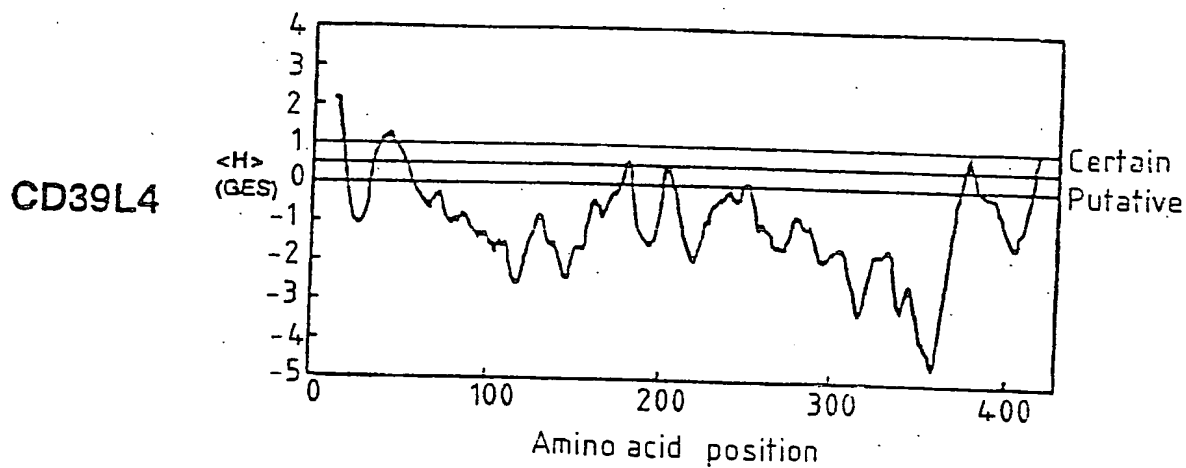


FIG. 5E





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ACCCACGGGT CTGGCCGGG GCCGCCTCTG CGGCAGCGGT AGTCGCCTTC TCCGAATCGG 60

CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT 112
Met Phe Thr Val Leu Thr Arg Gln Pro Cys 10
1 5

GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC 160
Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala 25
15 20

TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC 208
Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val 40
30 35

ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT 256
Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly 50
45 55

ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA 304
Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln 60
65 70

FIG. 6A



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TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC	352
Trp Pro Ala Glu Lys Glu Asn Thr Gly Val Ser Gln Thr Phe	90
75	85
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC	400
Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	105
95	100
caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg	448
Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	120
110	115
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	135
125	130
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	150
140	145
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	170
155	160

FIG. 6B

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FIG. 6C

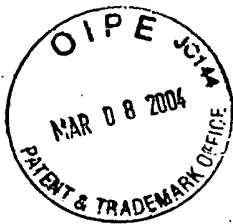
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	185
	175
	180
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	200
	190
	195
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	215
	205
	210
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	230
	225
ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	250
	240
	245
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	265
	255
	260



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GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	350 355 360	1168

FIG. 6D



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ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT 1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 375
365 370

GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC 1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 390
380 385

ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC 1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu 400
395 405

CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC 1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 420
415 425

TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT 1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 435
430 440

TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC 1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 450
445 455



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TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA	1504
Trp Ser Leu Gly Tyr Met	465
Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu	470
	475
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC	1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr	480
	485
	490
CTC GCT TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	495
	500
	505
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	510
	515
	520
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTCA AAGCAGCTCC TGGAGTCCAA	1699
Asp His Ala Val Asp Ser Asp	525
TGGCTGCTTA GAGTCAGCCT GGGTGGCACC AGGCAATGCA GTGAAGTGG CTGCCTTCAG	1759

FIG. 6F



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GAAATACAAC TAACTAAAAT CAAACACCTA GGTACAGTGC CTCTCAAATA CTGATTCTTG 1819
CCACAGCACC TCTTGAGGCA TCCCTTGGCT ATTCTGTGCA TATTGTTCTT CAGAGACCTC 1879
ACTACCCACA TGCTGATCTA TTGGGGAACA GAGAAGAGAC AGGCCACTAA GGTCAGGCTC 1939
TTTATATTAA GTTCCCCAGA GGAAGAGTAA GTTGAGAAGG TATCAGTTTA ATGTTGAAGA 1999
ATTGACCTCA GGGCTCAGTT TCCATTCCC TCCCTCAGTA TTCTTCCTGG CAAGATACCC 2059
ATTAAGCAAT TCGCCAAATCA GAATCTCAT TTTATAGTTTT TCCCATTTGG CTTTAACTAA 2119
GACTTTCTTG TAGCAATCTC GTAAGCAGTG AACCCCTCA GATCAGTAGA ATATAGTATC 2179
TGGGGGAGAA GACTTACTTC CTTCAGGGCA GCAGCCACAG CCAGGCTTCT GTCATACAGG 2239
TAGATCCCGA AGCACAGAGA CATAAAAAG GTCTCCCAGA AAATATAGA CCATTCTCCA 2299
AGTGAATTC CCACTTAGGG CTCGTGGTAC TAGATTGCAA CCTGTGTGTT TGTATCATC 2359
CTCATCTCAC CATTGTATTG CTATGCCCTC CCATAAAAC ACATTGATCC CTAGCAAGAT 2419



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TATTGCATT CAGATTTTAC TGCCTTTGCT AGGCTTTTGC TTAGCAAAGG GCTGACTTTC 2479
CATTGTTATC ATGGTGTATA TATTTTGTG ACCATTCCCA CAAGTATACT TGATGTTGTC 2539
ATAGAACGAA CATCCTACTC TATGATTTAC TAACCAATTA CTTTCCCGA TCATAGACCT 2599
CTCTGCATAG TAGTCATAGG TCTTGAÇTTT GGGGAAAGAA AAGGAAGCTG CAGGAATATT 2659
TATCTCCAAA GTCGAATGAG AAAGAACTCC AGCAAATCCA ATGGCTACAA ACTAAAAATC 2719
AGCATTATTT CATATTGCTG TTTCTTAGCT GAATATGGAA TAAAGAACTA TTATTTTATT 2779
TTGAAAAAAA AAAAAAAA 2797

FIG. 6H



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FIG. 7A

GGCGCGCGGT TTTCCCTTGTT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC 60
TCATACAGAC AAGATCATT TGGTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTG 120
AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTCAGA AGGAAAGAAA AAATTGCCCTC 180
TGCAGGTGTG CGAGCAGGAT TGCTTCTGCA ACAAAGCCT CCACCCAGCC ACATCTTGGG 240
AAAAAG ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
1 5 10
TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Thr Trp Phe
15 20 25 30
GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
35 40 45
ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
50 55 60



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CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA	480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu	
65	70
	75
GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA	528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val	
80	90
	95
GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG	576
Asp Gln Pro Lys Gln Ala Glu Thr Val Gln Gly Leu Leu Glu Val	
95	100
	105
GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC	624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val	
115	120
	125
CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG	672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys	
130	135
	140
GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG	720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu	
145	150
	155



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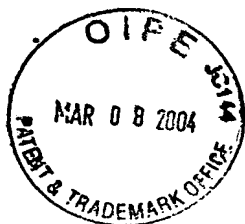
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FIG. 7C

GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA	768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile	
160 165 170	
TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC	816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His	
175 180 185 190	
AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA	864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln	
195 200 205	
ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG	912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg	
210 215 220	
GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT	960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr	
225 230 235	
ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	



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CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	255 260 265 270
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	275 280 285
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC	1152
Lys Tyr Gln Tyr Glu Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	290 295 300
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	305 310 315
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	320 325 330
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA	1296
Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu	335 340 345 350

FIG. 7D



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AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG 1344
Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu 365
355 360

GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC 1392
Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr 380
370 375

ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC 1440
Ile Thr Ala Leu Leu Lys Asp Gly Phe Phe Ala Asp Ser Thr Val 395
385 390

TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG 1488
Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu 410
400 405

GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT 1530
Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 425
415 420

TGAGGCCACG TACTTCCTTG GAGACCTGCA TTGCGCAACA CCTTTTAAAG GGGAGGAGAG 1590



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AGCACTTAGT TTCTGAACTA GTCTGGGACA TCCTGGACTT GAGCCTAGAG ATTTAGGTTT 1650
AATTAAATTT ACACATCTAA TGTGAACTGC TGCCTAACCA CTCAGAGTA CACAGCTGGC 1710
ACCAGAGCAT CACAGAGAGC CCTGTGAGCC AAAAAGTATA GTTTTGGAAC TTAACCTTGG 1770
AGTGAGAGCC CAGGGACAGG TCCCTGGAAA CCAAAGAAAA ATCGCATTTC AACCCTTTGA 1830
GTGCCTCATT CCACTGAATA TTAAATTTT CCTCTTAAAT GGTAAACTGA CTTATTGCAA 1890
TCCCAAGACC CATCAATATC AGTATTTTTT TCCTCCCCTAT ACAGTGCCCTT GCCCACCCCTT 1950
ATCTGCACCC ACCTCCCCCTG AAAAAGAGAG AAAAAAAAAA AAAAAAAA 1998

FIG. 7F



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CD39L2	1	MKKGIRYETSRKTSYIFQQPQHGPNQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI	
CD39L4	1	-----	
CD39L1	1	-----MATSWG	
CD39L3	1	-----	
CD39	1	-----MFTVLTRQPCQAGL	
		-----MEDTKE	
CD39L2	61	KWHRATATQAFFSITRAAPGARWGQAH-SPLGTAADGHEVFYGINF	ACR I
CD39L4	7	TVFFMLVSCVCSAVSHRNQQTWFEIGIFLSSMCPINVSASTLYGINF	DAGSTGTRVHVFPQ
CD39L1	1	---MAGKVRSLPPLLAAAGLAGLLLCVPTRDVREP?ALKYGIVL	DAGSTGTRI HVYT
CD39L3	16	KALYRTPTIIALVVLVLSIVVLVSTVVIQIHKQEVLP-PGGLKYGIVL	DAGSSHTSMFIYK
CD39	7	SNVKTFCSKNILAILGFSIIAIVIALLAAGLTONKALPENVKYGIVL	DAGSSRTTVVYVQ
			DAGSSHTSLYIYK
CD39L2	120	FT-RPPRETPTLTHTFKAVK-PGLSAYADDVEKSAQGIRELDDVAKQDIPFDFWKATPL	ACR II
CD39L4	67	FVQKMPGQLPILEGEVFDVSK-PGLSAFVDQPKQGAETVQGLLEVAKDSIPRSHWKKTPV	
CD39L1	58	WPADKENDTGIVGQHSSCDVPGGGISSYADNP SGASQSLVGCLEQALQDVPKERHAGTPL	
CD39L3	75	WPAEKENNTGVVSQTFKCSVKSGSISSYGNPNQDVPRAFECECMQKVKGQVPSHLHGSTPI	
CD39	67	WPAEKENDTGVVHQVEECRAVKGPGISKFVKVNEIGIYLTDCMERAREVIPRSQHQETPV	

FIG. 8A



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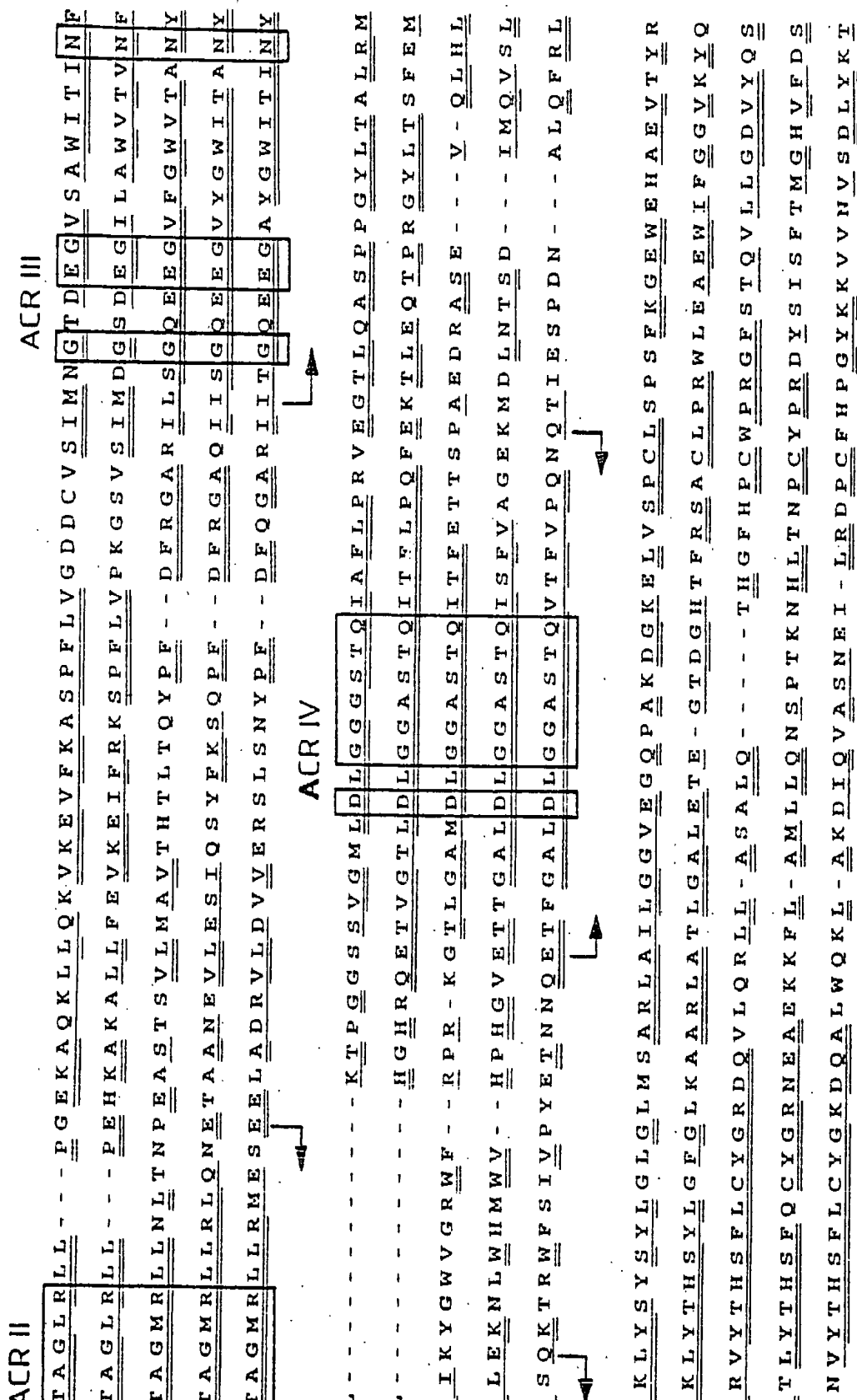
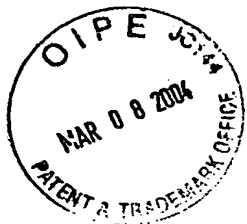


FIG. 8B



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CD39L2 343 VSGQAAASLHELCAARVSEVLQNRVHRTEEVKHVDFFYAFSYYDLAAGVGLIDAEEKGGS

CD39L4 290 YGGNQEGEVGFEPCEYAEVLRVVRGKHLHQPEEVQSGSFYAFSYYDRAVDTDMDIYEKGGI

CD39L1 283 PCTMAQRPQNFNSARVSLSGSSDPHLRCRDLVSGLFSFSSC-PFSRCSFNGVFQPPVAGN

CD39L3 307 LCTVDQRPESYNPNNDVITFEGTGDPSSLCKEKVASIFDFKACHDQETCSFDGYYQPKIKGP

CD39 300 PCT--KRFEMTLPFQQFEIQGIGNYQQCHQSILELFNTSYC-PYSQCAFNGIFLPPPLQGD

CD39L2 403 LVVGDFEIAAKYVCRLETQPQSSPFS CMDLTYVSLLLQE-FGFPRSKVLKLTTRKIDNVE

CD39L4 350 LKVEDFERKAREVCDNLENFTSGSPFLCMDLSYITALLKDGFGFADSTVLQLTKKVNNE

CD39L1 342 FV-----AFSAFFYTVDFLRTSMGLPVATLQQLEAAAVNVCNQTTAQ-----

CD39L3 367 FV-----AFAGFYTTASALNLSGSF--SLDTFNSSTWNFCSQNWSQLPLLPKFDEVY

CD39 357 FG-----AFSAFYFVMKFLNLT--EKVSQEKVTEMKKKFCAPWEEIKTSYAGVKEKY

CD39L2 462 TSWALGAI FHYIDS LNRQKSPAS*

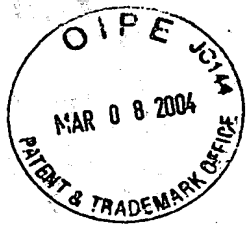
CD39L4 410 TGWA LGATFHL LQSLGISH

CD39L1 384 -----QLLSRGYGFDERAFGGVIFQKKAADTAVGWA LGYMLNLTNLI PADPPG

CD39L3 418 ARSYCF SANIYIYHLFVNGYKPTTEETWPQIHFEKEVGNSSIAWS LGYMLSLTNQIPAESPL

CD39 409 LSEYCFSGTYILSLLLOGYHFTADSWEHIHFIGIKIQGSDAGWTLGYMLNLTNMIPAEQP-

FIG. 8C



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CD39L2 485
CD39L4 429
CD39L1 432 LRKGTDPSSWVVLLLLFASALLAALVLLLRQVHSAKLPSTI*
CD39L3 478 IRLPIEPPVFVGTLAFFTVAALCLAFLAYLCSATRRKRRRHSEHAFDHAVDSD*
CD39 468 LSTPLSHSTYVFLMVLFSLVLFTVAIGIGLLIFIHKPSYFWKDMV*

FIG. 8D



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peaGDP	1	-----M
potapyrase 1	1	-----MLNQN
CD39L2	1	MKKGIRYETSRKTSYIFQQPQHGPWQTRMRKISNHGSLRVAKVAYPLGLCVGVFIYVAYI
CD39L4	1	-----MATSWG
dNTPase	1	-----MKY EYKLLATDEKPPRRKSSGSPNASGGNRGPSGL
YGD Pase	1	-----KTPE
peaGDP	2	ELLIKLIITFLFSPAITSSQYLGNNL-LTSRKIFLKQEEISSYAVVF
potapyrase 6	6	SHFIFIILAI FLVLP LSLSKNVNAQI-PLRRHL LSHSE- -HYAVIF DAGSTGSRVHVF
CD39L2	61	KWHRATATQAFFSITRAAPGARWGQQA-H-SPIGTAADGHEVFFYGIMFF DAGSTGTRVHVF
CD39L4	7	TVFFMLVVSVCVCSAVSHRNQQTWFEGI-FLSSMCPINVSASTLYGIMFF DAGSTGTRIHVY
dNTPase	37	KISFLCLIIISVILLFLVFGFVSENASP-YLLARLASKFGYSKVQYAAIIDAGSTGSRVLAY
YGD Pase	5	DISILPVNDEPGYLQDSKTEQNYPELADAVKQTSQTCSEENK YVIMIDAGSTGSRVHIY

ACRI

FIG. 9A



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		ACR II	
peaGDP	61	HFNQNLDDLHIGKGV EY YNK I T P G L S S Y A N N P E Q A A K S L I P L L E Q A E D V V P D D L Q P K T P V	
potapyrase	63	RFDEKLG L L P I G N N I E Y F M A T E P G L S S Y A E D P K A A A N S L E P L L D G A E G V V P Q E L Q S E T P L	
CD39L2	119	Q F T - R P P R E T P T L T H E T F K A V K P G L S A Y A D D V E K S A Q G I R E L L D V A K Q D I P F D F W K A T P L	
CD39L4	66	T F V Q K M P G Q L P I L E G E V F D S V K P G L S A F V D Q P K Q G A E T V Q G L L E V A K D S I P R S H W K K T P V	
dNTPase	96	K F N R S F I D N K K L V L Y E E L F F K E R K P G L S S F A D N P A E G A H S I K L L D E A R A F I P K E H W S S T P L	
YGDpase	65	K F D - - V C T S P P T L L D E K F D M L E P G L S S F D T D S V G A A N S L D P L L K V A M N Y V P I K A R S C T P V	
		ACR III	
peaGDP	121	R L G A T A G L R L L N G D A S E K I L Q S V R D M L S N R S T F - N V Q P D A V S I I D G T Q E G S Y L W V T V N Y A	
potapyrase	123	E L G A T A G L R M L K G D A A E K I L Q A V R N L V K N Q S T F - H S K D Q W V T I L D G T Q E G S Y M W A A I N Y L	
CD39L2	178	V L K A T A G L R L L P G E K A Q X L L Q K V K E V F K - A S P F - L V G D D C V S I M N G T D E G V S A W I T I N F L	
CD39L4	126	V L K A T A G L R L L P E N H K A K A L L F E V K E I F R - K S P F - L V P K G S V S I M D G S D E G I L A W V T V N F L	
dNTPase	156	V L K A T A G L R L L P A S K A E N I L N A V R D L F A - K S E F - S V D M D A V E I M D G T D E G I F S W F T V N F L	
YGDpase	123	A V K A T A G L R L L G D A K S S K I L S A V R D H L E K D Y P F P V V E G D G V S I M G G D E E G V F A W I T T N Y L	

FIG. 9B

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ACRIV

peaGDP	180	LGNLGKKYTK--TVGVI	DLGGGSVQ	MAYAVSKKTAKNAPKVADGDDPYIKKVVVLKGI	PYD
potapyrase	182	LGNLGKDYKS--TTATI	DLGGGSVQ	MAYAIISNEQFAKAPONEDG-EPYVQQKHLMSKDY	YN
CD39L2	236	TGSLKTPGGS--SVGML	DLGGGSSTQ	IAFLPRVEG-----TLQASPPGYLTALRMFNRTYK	
CD39L4	184	TGQLHGHQRQE--TVGTL	DLGGASTQ	ITFLPOFEK-----TLEQTPRGYLTSEFMPNSTYK	
dNTPase	214	LGRISKTNQA--AA--LD	DLGGGSSTQ	VTFSPTDPD-----QVPVYDK-YMHEVVTSKKIN	
YGD Pase	183	LGNIGANGPKLPTAAVFF	DLGGGSSTQ	IVPEPTFPINEKMOV-----DGEHKFDLXFGDENYT	

peaGDP	238	LYVHSYLFHFGREASRAEILKLT	PRSP	-----NPCLLAGFNG	-----LY
potapyrase	239	LYVHSYLNXYGQLAGRAEIFKAS	RNES	-----NPCALEGCDG	-----YY
CD39L2	289	LYSYSYLGGLMSARLAILGGVEG	QPAKDGKELV	-----SPCLSPSPFKG	-----E-W
CD39L4	237	LYTHSYLGFGGLKAARLATLGA	LETE	-----SACLPRWLEA	-----E-W
dNTPase	264	VFTHSYLGGLMAARHAAVF--	---THGYKKEDTVLE	-----SVCVNPIIAN	-----RTW
YGD Pase	238	LYQFSHLGYGLKEGRNKNVNSV	LVENALKDGI	LLKGDNTKTHQLSSPCLPPK	VNA

FIG. 9C



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peaGDP	276	<u>TYSGEEFKATAYTSG-ANFNKCKNTIRKALKLNYPYQYONCTFGGIWNGG</u> ---GGNGQKN
potapyrase	277	<u>SYGGVDYKVKAPKKG-SSWKRCLTRHALKINAKCNIEECTFNGVWNGG</u> ---GGDGQKN
CD39L2	335	<u>EHAETVYRVSGQKAAASLHELCAAR</u> ---VSEV---LQNRV---HRT---EEVKHVD
CD39L4	282	<u>IFGGVKYQYGGNQEGEVGFPCYAE</u> ---VLRV---VRGKL---HQP---EEVQGRGS
dNTPase	308	<u>TYGNVQYKVSQKENGKSSAEQPIVDFDACLEL</u> ---VKSKVMPLVKPKP---FTLKQHA
YGD Pase	298	<u>LESKETYTIDFIGPDEPSSGAQCRFLTDEILNKKDAQCSPPCSFNGVHQPSLVRTPKESND</u>
peaGDP	332	<u>LFASSSFFYLPEDTGMVDASTPNFILLRPVDIETKAKEACALNFEDAKSTYPFLDKKNVAS</u>
potapyrase	333	<u>IHASFFFYDIGAQVGI VDTKFPSSALAKPIQYLNAAKVACQTNVADIKSIFPKTQDRNI-P</u>
CD39L2	379	<u>FYAFSYYYDLAAGVGLIDAE-KGGSLLVVGDPFEIAAKYVCRT</u> ---LETQPQSSP
CD39L4	326	<u>FYAFSYYYDRAVDTDMIDYE-KGGILKVEDFERKAREVCDN</u> ---LENFTSGSP
dNTPase	360	<u>VAAFSYYFERRAIESGLVDPL-AGGETTVEAYRKKAEICAI</u> ---PNDE---QP
YGD Pase	358	<u>IYIFSYFYDTRTRPLGMPLSFTLNELNDLARI VCKGEEETWNSVFSGIAGSL</u> ---DELESDS

FIG. 9D



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peaGDP	392	<u>YV</u> <u>CMD</u> <u>L</u> <u>I</u> <u>YQ</u> <u>V</u> <u>L</u> <u>L</u> <u>V</u> <u>D</u> <u>G</u> <u>F</u> <u>G</u> <u>L</u> <u>D</u> <u>P</u> <u>L</u> <u>Q</u> <u>K</u> <u>I</u> <u>T</u> <u>S</u> <u>G</u> <u>K</u> <u>E</u> <u>I</u> <u>E</u> <u>Y</u> <u>Q</u> <u>D</u> <u>A</u> <u>I</u> <u>V</u> <u>E</u> <u>A</u> <u>A</u> <u>P</u> <u>L</u> <u>G</u> <u>N</u> <u>A</u> <u>V</u> <u>E</u> <u>A</u> <u>I</u> <u>S</u> <u>A</u> <u>L</u> <u>P</u> <u>K</u> <u>F</u> <u>E</u> <u>R</u> <u>L</u>
potapyrase	392	<u>Y</u> <u>L</u> <u>C</u> <u>M</u> <u>D</u> <u>L</u> <u>I</u> <u>Y</u> <u>E</u> <u>Y</u> <u>T</u> <u>L</u> <u>L</u> <u>V</u> <u>D</u> <u>G</u> <u>F</u> <u>G</u> <u>L</u> <u>N</u> <u>P</u> <u>H</u> <u>K</u> <u>E</u> <u>I</u> <u>T</u> <u>V</u> <u>I</u> <u>H</u> <u>D</u> <u>V</u> <u>Q</u> <u>Y</u> <u>K</u> <u>N</u> <u>Y</u> <u>L</u> <u>V</u> <u>G</u> <u>A</u> <u>A</u> <u>P</u> <u>L</u> <u>G</u> <u>C</u> <u>A</u> <u>I</u> <u>D</u> <u>L</u> <u>V</u> <u>S</u> <u>S</u> <u>T</u> <u>T</u> <u>N</u> <u>K</u> <u>I</u> <u>R</u> <u>V</u>
CD39L2	428	<u>F</u> <u>S</u> <u>C</u> <u>M</u> <u>D</u> <u>L</u> <u>T</u> <u>Y</u> <u>V</u> <u>S</u> <u>L</u> <u>L</u> <u>Q</u> <u>E</u> <u>-</u> <u>P</u> <u>G</u> <u>F</u> <u>P</u> <u>R</u> <u>S</u> <u>K</u> <u>V</u> <u>L</u> <u>K</u> <u>L</u> <u>T</u> <u>R</u> <u>K</u> <u>I</u> <u>D</u> <u>N</u> <u>-</u> <u>-</u> <u>-</u> <u>V</u> <u>E</u> <u>T</u> <u>S</u> <u>W</u> <u>A</u> <u>L</u> <u>G</u> <u>A</u> <u>I</u> <u>F</u> <u>H</u> <u>Y</u> <u>I</u> <u>D</u> <u>S</u> <u>L</u> <u>N</u> <u>R</u> <u>Q</u> <u>K</u> <u>S</u> <u>P</u>
CD39L4	375	<u>F</u> <u>L</u> <u>C</u> <u>M</u> <u>D</u> <u>L</u> <u>S</u> <u>Y</u> <u>I</u> <u>T</u> <u>A</u> <u>L</u> <u>L</u> <u>K</u> <u>D</u> <u>G</u> <u>F</u> <u>G</u> <u>F</u> <u>A</u> <u>D</u> <u>S</u> <u>T</u> <u>V</u> <u>L</u> <u>Q</u> <u>L</u> <u>T</u> <u>K</u> <u>K</u> <u>V</u> <u>N</u> <u>N</u> <u>-</u> <u>-</u> <u>-</u> <u>I</u> <u>E</u> <u>T</u> <u>G</u> <u>W</u> <u>A</u> <u>L</u> <u>G</u> <u>A</u> <u>T</u> <u>F</u> <u>H</u> <u>L</u> <u>L</u> <u>Q</u> <u>S</u> <u>L</u> <u>G</u> <u>I</u> <u>S</u> <u>H</u>
dNTPase	406	<u>F</u> <u>M</u> <u>C</u> <u>F</u> <u>D</u> <u>L</u> <u>T</u> <u>F</u> <u>I</u> <u>S</u> <u>T</u> <u>L</u> <u>L</u> <u>R</u> <u>E</u> <u>G</u> <u>F</u> <u>G</u> <u>L</u> <u>N</u> <u>D</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>K</u> <u>L</u> <u>Y</u> <u>K</u> <u>K</u> <u>I</u> <u>D</u> <u>G</u> <u>-</u> <u>-</u> <u>-</u> <u>H</u> <u>E</u> <u>I</u> <u>S</u> <u>W</u> <u>A</u> <u>L</u> <u>G</u> <u>C</u> <u>A</u> <u>Y</u> <u>N</u> <u>V</u> <u>L</u> <u>T</u> <u>S</u> <u>D</u> <u>E</u> <u>K</u> <u>F</u> <u>S</u> <u>N</u> <u>S</u>
YGDpase	415	<u>H</u> <u>F</u> <u>C</u> <u>L</u> <u>D</u> <u>L</u> <u>S</u> <u>F</u> <u>Q</u> <u>V</u> <u>S</u> <u>L</u> <u>L</u> <u>H</u> <u>T</u> <u>G</u> <u>Y</u> <u>D</u> <u>I</u> <u>P</u> <u>L</u> <u>Q</u> <u>R</u> <u>E</u> <u>L</u> <u>R</u> <u>T</u> <u>G</u> <u>K</u> <u>K</u> <u>I</u> <u>A</u> <u>N</u> <u>K</u> <u>-</u> <u>-</u> <u>-</u> <u>E</u> <u>I</u> <u>G</u> <u>W</u> <u>C</u> <u>L</u> <u>G</u> <u>A</u> <u>S</u> <u>L</u> <u>P</u> <u>L</u> <u>L</u> <u>K</u> <u>A</u> <u>D</u> <u>N</u> <u>W</u> <u>K</u> <u>C</u> <u>K</u> <u>I</u>
peaGDP	452	<u>M</u> <u>Y</u> <u>F</u> <u>V</u>
potapyrase	452	<u>A</u> <u>S</u> <u>S</u> <u>*</u>
CD39L2	483	<u>A</u> <u>S</u> <u>*</u>
CD39L4	429	
dNTPase	462	
YGDpase	471	<u>Q</u> <u>S</u> <u>A</u>

FIG. 9E